

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.

Application Serial Number: 10/608,388A  
Source: IFWO  
Date Processed by STIC: 11/23/04

# ***ENTERED***



IFWO

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/608,388A

DATE: 11/23/2004

TIME: 14:28:38

Input Set : A:\11-17-2004-Seq List.txt

Output Set: N:\CRF4\11222004\J608388A.raw

```

3 <110> APPLICANT: KATO, Seishi
4     SEKINE, Shingo
5     YAMAGUCHI, Tomoko
7 <120> TITLE OF INVENTION: HUMAN MEMBRANE ANTIGEN TM4 SUPERFAMILY PROTEIN AND DNA
8     ENCODING THIS PROTEIN
10 <130> FILE REFERENCE: 2003-0907/WMC/01791
12 <140> CURRENT APPLICATION NUMBER: 10/608,388A
13 <141> CURRENT FILING DATE: 2003-06-30
15 <150> PRIOR APPLICATION NUMBER: 059571/1996
16 <151> PRIOR FILING DATE: 1996-03-15
18 <160> NUMBER OF SEQ ID NOS: 2
20 <170> SOFTWARE: PatenIn Version 2.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 759
24 <212> TYPE: DNA
25 <213> ORGANISM: Artificial Sequence
27 <220> FEATURE:
28 <223> OTHER INFORMATION: Human membrane antigen TM4 superfamily protein
30 <400> SEQUENCE: 1
33 atg ggc cag tgc ggc atc acc tcc tcc aag acc gtg ctg gtc ttt ctc 48
36 Met Gly Gln Cys Gly Ile Thr Ser Ser Lys Thr Val Leu Val Phe Leu
37 1 5 10 15
39 aac ctc atc ttc tgg ggg gca gct ggc att tta tgc tat gtg gga gcc 96
42 Asn Leu Ile Phe Trp Gly Ala Ala Gly Ile Leu Cys Tyr Val Gly Ala
43 20 25 30
45 tat gtc ttc atc act tat gat gac tat gac cac ttc ttt gaa gat gtg 144
48 Tyr Val Phe Ile Thr Tyr Asp Asp Tyr Asp His Phe Phe Glu Asp Val
49 35 40 45
51 tac acg ctc atc cct gct gta gtg atc ata gct gta gga gcc ctg ctt 192
54 Tyr Thr Leu Ile Pro Ala Val Val Ile Ile Ala Val Gly Ala Leu Leu
55 50 55 60
57 ttc atc att ggg cta att ggc tgc tgt gcc aca atc cgg gaa agt cgc 240
60 Phe Ile Ile Gly Leu Ile Gly Cys Cys Ala Thr Ile Arg Glu Ser Arg
61 65 70 75 80
63 tgt gga ctt gcc acg ttt gtc atc atc ctg ctc ttg gtt ttt gtc aca 288
66 Cys Gly Leu Ala Thr Phe Val Ile Ile Leu Leu Val Phe Val Thr
67 85 90 95
69 gaa gtt gtt gta gtg gtt ttg gga tat gtt tac aga gca aag gtg gaa 336
72 Glu Val Val Val Val Val Leu Gly Tyr Val Tyr Arg Ala Lys Val Glu
73 100 105 110
75 aat gag gtt gat cgc agc att cag aaa gtg tat aag acc tac aat gga 384
78 Asn Glu Val Asp Arg Ser Ile Gln Lys Val Tyr Lys Thr Tyr Asn Gly
79 115 120 125

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81 acc aac cct gat gct gct agc cgg gct att gat tat gta cag aga cag      432
84 Thr Asn Pro Asp Ala Ala Ser Arg Ala Ile Asp Tyr Val Gln Arg Gln
85      130      135      140
87 ctg cat tgt tgt gga att cac aac tac tca gac tgg gaa aat aca gat      480
90 Leu His Cys Cys Gly Ile His Asn Tyr Ser Asp Trp Glu Asn Thr Asp
91 145      150      155      160
93 tgg ttc aaa gaa acc aaa aac cag agt gtc cct ctt agc tgc tgc aga      528
96 Trp Phe Lys Glu Thr Lys Asn Gln Ser Val Pro Leu Ser Cys Cys Arg
97      165      170      175
99 gag act gcc agc aat tgt aat ggc agc ctg gcc cac cct tcc gac ctc      576
102 Glu Thr Ala Ser Asn Cys Asn Gly Ser Leu Ala His Pro Ser Asp Leu
103      180      185      190
105 tat gct gag ggg tgt gag gct cta gta gtg aag aag cta caa gaa atc      624
108 Tyr Ala Glu Gly Cys Glu Ala Leu Val Val Lys Lys Leu Gln Glu Ile
109      195      200      205
111 atg atg cat gtg atc tgg gcc gca ctg gca ttt gca gct att cag ctg      672
114 Met Met His Val Ile Trp Ala Ala Leu Ala Phe Ala Ala Ile Gln Leu
115      210      215      220
117 ctg ggc atg ctg tgt gct tgc atc gtg ttg tgc aga agg agt aga gat      720
120 Leu Gly Met Leu Cys Ala Cys Ile Val Leu Cys Arg Arg Ser Arg Asp
121 225      230      235      240
123 cct gct tac gag ctc ctc atc act ggc gga acc tat gca      759
126 Pro Ala Tyr Glu Leu Leu Ile Thr Gly Gly Thr Tyr Ala
127      245      250
129 <210> SEQ ID NO: 2
130 <211> LENGTH: 1722
131 <212> TYPE: DNA
132 <213> ORGANISM: Artificial Sequence
134 <220> FEATURE:
135 <223> OTHER INFORMATION: Human membrane antigen TM4 superfamily protein
138 <400> SEQUENCE: 2
140 acttgcctggg gtcggggctg cgcgacggcg caggggctgc ggggagcgcc ggcgaggccg 60
142 tgcagttcct agcgaggagg cgcgcgcgcc attgccgctc tctcggtgag cgcagccccg 120
144 ctctccgggc cgggccttcg cgggccaccg gcgcc atg ggc cag tgc ggc atc 173
146      Met Gly Gln Cys Gly Ile
147      1      5
149 acc tcc tcc aag acc gtg ctg gtc ttt ctc aac ctc atc ttc tgg ggg      221
152 Thr Ser Ser Lys Thr Val Leu Val Phe Leu Asn Leu Ile Phe Trp Gly
153      10      15      20
155 gca gct ggc att tta tgc tat gtg gga gcc tat gtc ttc atc act tat      269
158 Ala Ala Gly Ile Leu Cys Tyr Val Gly Ala Tyr Val Phe Ile Thr Tyr
159      25      30      35
161 gat gac tat gac cac ttc ttt gaa gat gtg tac acg ctc atc cct gct      317
164 Asp Asp Tyr Asp His Phe Phe Glu Asp Val Tyr Thr Leu Ile Pro Ala
165      40      45      50
167 gta gtg atc ata gct gta gga gcc ctg ctt ttc atc att ggg cta att      365
170 Val Val Ile Ile Ala Val Gly Ala Leu Leu Phe Ile Ile Gly Leu Ile
171 55      60      65      70
173 ggc tgc tgt gcc aca atc cgg gaa agt cgc tgt gga ctt gcc acg ttt      413

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176 Gly Cys Cys Ala Thr Ile Arg Glu Ser Arg Cys Gly Leu Ala Thr Phe
177              75              80              85
179 gtc atc atc ctg ctc ttg gtt ttt gtc aca gaa gtt gtt gta gtg gtt      461
182 Val Ile Ile Leu Leu Val Phe Val Thr Glu Val Val Val Val Val
183              90              95              100
185 ttg gga tat gtt tac aga gca aag gtg gaa aat gag gtt gat cgc agc      509
188 Leu Gly Tyr Val Tyr Arg Ala Lys Val Glu Asn Glu Val Asp Arg Ser
189              105              110              115
191 att cag aaa gtg tat aag acc tac aat gga acc aac cct gat gct gct      557
194 Ile Gln Lys Val Tyr Lys Thr Tyr Asn Gly Thr Asn Pro Asp Ala Ala
195              120              125              130
197 agc cgg gct att gat tat gta cag aga cag ctg cat tgt tgt gga att      605
200 Ser Arg Ala Ile Asp Tyr Val Gln Arg Gln Leu His Cys Cys Gly Ile
201 135              140              145              150
203 cac aac tac tca gac tgg gaa aat aca gat tgg ttc aaa gaa acc aaa      653
206 His Asn Tyr Ser Asp Trp Glu Asn Thr Asp Trp Phe Lys Glu Thr Lys
207              155              160              165
209 aac cag agt gtc cct ctt agc tgc tgc aga gag act gcc agc aat tgt      701
212 Asn Gln Ser Val Pro Leu Ser Cys Cys Arg Glu Thr Ala Ser Asn Cys
213              170              175              180
215 aat ggc agc ctg gcc cac cct tcc gac ctc tat gct gag ggg tgt gag      749
218 Asn Gly Ser Leu Ala His Pro Ser Asp Leu Tyr Ala Glu Gly Cys Glu
219              185              190              195
221 gct cta gta gtg aag aag cta caa gaa atc atg atg cat gtg atc tgg      797
224 Ala Leu Val Val Lys Lys Leu Gln Glu Ile Met Met His Val Ile Trp
225              200              205              210
227 gcc gca ctg gca ttt gca gct att cag ctg ctg ggc atg ctg tgt gct      845
230 Ala Ala Leu Ala Phe Ala Ala Ile Gln Leu Leu Gly Met Leu Cys Ala
231 215              220              225              230
233 tgc atc gtg ttg tgc aga agg agt aga gat cct gct tac gag ctc ctc      893
236 Cys Ile Val Leu Cys Arg Arg Ser Arg Asp Pro Ala Tyr Glu Leu Leu
237              235              240              245
239 atc act ggc gga acc tat gca tagttgacaa ctcaagcctg agcttt      940
241 Ile Thr Gly Gly Thr Tyr Ala
242              250
244 ttggtcttgt tctgatttgg aaggtgaatt gagcaggtct gctgctgttg gcctctggag      1000
246 ttcatttagt taaagcacat gtacactggg gttggacaga gcagcttggc ttttcatgtg      1060
248 cccacctact tacctactac ctgcgacttt ctttttcctt gttctagctg actcttcatg      1120
250 cccctaagat tttaagtacg atggtgaacg ttctaatttc agaaccaatt gcgagtcag      1180
252 tagtggtgta gaattaaagg aggacacgag cctgcttctg ttacctcaa gtggtaacag      1240
254 gactgatgcc gaaatgtcac caggtccttt cagtcttcac agtggagaac tcttggccaa      1300
256 aggtttttgc ggggaggagg aggaaaccag ctttctggtt aaggttaaca ccagatggtg      1360
258 cccctcattg gtgtcctttt aaaaaatatt tactgtagtc caataagata gcagctgtac      1420
260 aaaatgacta aaatagattg taggatcata tggcgtatat cttggttcat cttcaaaatc      1480
262 agagactgag ctttgaaact agtgggtttt aatcaaagtt ggctttatag gaggagtata      1540
264 atgtatgcac tactgtttta aaagaattag tgtgagtgtg tttttgtatg aatgagccca      1600
266 ttcatggtaa gtcttaagct tgttggaat aatgtacca tgtagactag caaaatagta      1660
268 tgtagatgtg atctcagttg taaatagaaa aatctaattc aataaactct gtatcagccc      1720
270 cc

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